

<110> APPLICANT: Keith G. Weinstock et al.
 <120> TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROBACTER
 CLOACAE FOR DIAGNOSTICS AND THERAPEUTICS
 <130> FILE REFERENCE: 107196.135
 <140> CURRENT APPLICATION NUMBER: US/09/252,691C
 <141> CURRENT FILING DATE: 1999-02-18
 <150> PRIOR APPLICATION NUMBER: US 60/094,145
 <151> PRIOR FILING DATE: 1998-07-24
 <150> PRIOR APPLICATION NUMBER: US 60/074,787
 <151> PRIOR FILING DATE: 1998-02-18
 <160> NUMBER OF SEQ ID NOS: 11326

<210> SEQ ID NO 1394
 <211> LENGTH: 669
 <212> TYPE: DNA
 <213> ORGANISM: Enterobacter cloacae
 <400> SEQUENCE: 1394
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 agcgggtca tactgtcaa taaccctac gatgtatgc cgcagttac cgcagagcc
 ggcgcagca cgtgaagga ttattcccc gttcagggag tctacgcagc ggcagctctg
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 caggtcaggc gcatgactgc gcatgtggc ttccctaccc tgcactcat tgcctacgc
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<210> SEQ ID NO 7056
 <211> LENGTH: 222
 <212> TYPE: PRT
 <213> ORGANISM: Enterobacter cloacae
 <400> SEQUENCE: 7056
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 5 Ser Phe Arg Lys His Arg Val Glu Arg Phe Ser Ser Arg Gln Ala Thr
 10 Arg Arg Thr Pro Glu Pro Gln Pro Thr Arg Val Ile Leu Phe Asn Lys
 15 Pro Tyr Asp Val Leu Pro Gln Phe Thr Asp Glu Ala Gly Arg Ser Thr
 20 Leu Lys Asp Phe Ile Pro Val Gln Gly Val Tyr Ala Ala Gly Arg Leu
 25 Asp Arg Asp Ser Glu Gly Leu Leu Val Leu Thr Asn Asp Gly Val Leu
 30 Gln Ala Arg Leu Thr Gln Pro Gly Lys Arg Thr Gly Lys Ile Tyr Tyr
 35 Val Gln Val Glu Gly Glu Pro Asp Asp Ala Ser Leu Ala Lys Leu Arg
 40 Asn Gly Val Thr Leu Asn Asp Gly Pro Thr Leu Pro Ala Gly Ile Glu
 45 Arg Val Asn Glu Pro Glu Trp Leu Trp Pro Arg Asn Pro Pro Ile Arg
 50 Glu Arg Lys Ser Ile Pro Thr Ser Trp Leu Lys Ile Thr Leu Tyr Glu
 55 Gly Arg Asn Arg Gln Val Arg Arg Met Thr Ala His Val Gly Phe Pro
 60 Thr Leu Arg Leu Ile Arg Tyr Ala Met Gly Ser Tyr Thr Leu Asp Ser
 65 Leu Ala Asn Gly Glu Trp Arg Asp Val Thr Pro Lys Glu Asn
 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220

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ggcggtgta tactttcaa taaccttac gattattgc cgcagtttac gacagagcc
ggcgagaca cgtgaagga cttatcccc gttacaggag tctacgagc gggacgtctg
gacgcgaca gcgaggggt gctgtctct accaatgacg gcgtgctcca ggcagggctt
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gagctaaat caattctac cagttgctt aaatcaccc tttaagag ccgaacga
caggtcagc gcattgctg ctcctaccc tgcactacc tgcactacc tgcactacc
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gagaactga

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<212> TYPE: PRT
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1 5 10 15
Ser Phe Arg Lys His Arg Val Glu Arg Phe Ser Ser Arg Gln Ala Thr
20 25 30
Arg Arg Thr Pro Glu Pro Gln Pro Thr Arg Val Ile Leu Phe Asn Lys
35 40 45
Pro Tyr Asp Val Leu Pro Gln Phe Thr Asp Glu Ala Gly Arg Ser Thr
50 55 60
Leu Lys Asp Phe Ile Pro Val Gln Gly Val Tyr Ala Ala Gly Arg Leu
65 70 75 80
Asp Arg Asp Ser Glu Gly Leu Leu Val Leu Thr Asn Asp Gly Val Leu
95
Gln Ala Arg Leu Thr Gln Pro Gly Lys Arg Thr Gly Lys Ile Tyr Tyr
100 105 110
Val Gln Val Glu Gly Glu Pro Asp Ala Ser Leu Ala Lys Leu Arg
115 120 125
Asn Gly Val Thr Leu Asn Asp Gly Pro Thr Leu Pro Ala Gly Ile Glu
130 135 140
Arg Val Asn Glu Pro Glu Trp Leu Trp Pro Arg Asn Pro Pro Ile Arg
145 150 155 160
Glu Arg Lys Ser Ile Pro Thr Ser Trp Leu Lys Ile Thr Leu Tyr Glu
165 170 175
Gly Arg Asn Arg Gln Val Arg Arg Met Thr Ala His Val Gly Phe Pro
180 185 190
Thr Leu Arg Leu Ile Arg Tyr Ala Met Gly Ser Tyr Thr Leu Asp Ser
195 200 205
Leu Ala Asn Gly Glu Trp Arg Asp Val Thr Pro Lys Glu Asn
210 215 220

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acggggatca tactgttcaa taaccttac gatgtattgc cgcagtttac cgcagagccc 180
ggcgcaaga cgtgaaga ttattatccc gtacaggag tctacgcagc ggacggtctg 240
gatcgagca gcgagggtc gctgtctt accaatgac gctgtctca gccagagctt 300
actcagcgg gaacagctac cggaaaatt tactatgtc agttigaag cgcagcgac 360
gacgctcgc tggcaagct gcgaacggc gtaacgttga acgaggtccc caccctgcc 420
gctggattg aacgtgtgaa tgaacccgag tggctgtg cgcgaacccc gccattcgt 480
gagctaaat ccatctctac cagtggtctt aaatcacccc ttattgaagg ccgcaaccca 540
cagctcaggc gcattgactg ccatgtgggc ttccctaccc tgcgactcat tcgctaagcc 600
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gagaactga 669

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Ala Ile Met Arg Gln Leu Ile Thr Pro Glu Asn Thr Met Thr Lys Thr 15
1 Ser Phe Arg Lys His Arg Val Glu Arg Phe Ser Arg Gln Ala Thr 30
Arg Arg Thr Pro Glu Pro Gln Pro Thr Arg Val Ile Leu Phe Asn Lys 45
35 40 45
Pro Tyr Asp Val Leu Pro Gln Phe Thr Asp Glu Ala Gly Arg Ser Thr 60
50 55 60
Leu Lys Asp Phe Ile Pro Val Gln Gly Val Tyr Ala Ala Gly Arg Leu 75
65 70 75
Asp Arg Asp Ser Glu Gly Leu Leu Val Leu Thr Asn Asp Gly Val Leu 90
85 90 95
Gln Ala Arg Leu Thr Gln Pro Gly Lys Arg Thr Gly Lys Ile Tyr Tyr 110
100 105 110
Val Gln Val Glu Gly Glu Pro Asp Asp Ala Ser Leu Ala Lys Leu Arg 125
115 120 125
Asn Gly Val Thr Leu Asn Asp Gly Pro Thr Leu Pro Ala Gly Ile Glu 140
130 135 140
Arg Val Asn Glu Pro Glu Trp Leu Trp Pro Arg Asn Pro Pro Ile Arg 160
145 150 155 160
Glu Arg Lys Ser Ile Pro Thr Ser Trp Leu Lys Ile Thr Leu Tyr Glu 175
165 170 175
Gly Arg Asn Arg Gln Val Arg Arg Met Thr Ala His Val Gly Phe Pro 190
180 185 190
Thr Leu Arg Leu Ile Arg Tyr Ala Met Gly Ser Tyr Thr Leu Asp Ser 205
195 200 205
Leu Ala Asn Gly Glu Trp Arg Asp Val Thr Pro Lys Glu Asn 220
210 215 220

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cacg99gttg agcgattcag ctacgacaa gccaccagaa gaacccaga acccagcca
acg99gtca tactttcaa taaccctac gatatttc cagatttac cgaagggcc
ggcgagaca cgtgaagga cttatcccc gtacaggag tctacgagc gggacgtctg
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gagcgtaaat ccattcctac cagtggtctt aaatcaccc tttagaagg ccgcaacga
cagtcagcgc gcatgactgc gcatgtggc ttccctacc tgcactcat tcgtaacgc
atggcagct atacgtgga ctcgtggca aacggggaat ggcgggatgt tacccctaa
gagcactga

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1 5 10 15
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Arg Arg Thr Pro Glu Pro Gln Pro Thr Arg Val Ile Leu Phe Asn Lys
35 40 45
Pro Tyr Asp Val Leu Pro Gln Phe Thr Asp Glu Ala Gly Arg Ser Thr
50 55 60
Leu Lys Asp Phe Ile Pro Val Gln Gly Val Tyr Ala Ala Gly Arg Leu
65 70 75
Asp Arg Asp Ser Glu Gly Leu Leu Val Leu Thr Asn Asp Gly Val Leu
80 85 90
Gln Ala Arg Leu Thr Gln Pro Gly Lys Arg Thr Gly Lys Ile Tyr Tyr
100 105 110
Val Gln Val Glu Gly Glu Pro Asp Asp Ala Ser Leu Ala Lys Leu Arg
115 120 125
Asn Gly Val Thr Leu Asn Asp Gly Pro Thr Leu Pro Ala Gly Ile Glu
130 135 140
Arg Val Asn Glu Pro Glu Trp Leu Trp Pro Arg Asn Pro Pro Ile Arg
145 150 155
Glu Arg Lys Ser Ile Pro Thr Ser Trp Leu Lys Ile Thr Leu Tyr Glu
160 165 170
Gly Arg Asn Arg Gln Val Arg Arg Met Thr Ala His Val Gly Phe Pro
175 180 185
Thr Leu Arg Leu Ile Arg Tyr Ala Met Gly Ser Tyr Thr Leu Asp Ser
190 195 200
Leu Ala Asn Gly Glu Trp Arg Asp Val Thr Pro Lys Glu Asn
205 210 215 220